

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/750,262 A
Source: TFW/6
Date Processed by STIC: 03/23/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/23/2006

PATENT APPLICATION: US/10/750,262A

TIME: 15:22:29

Input Set : A:\PTO.TS.14.txt

Output Set: N:\CRF4\03232006\J750262A.raw

4 <110> APPLICANT: AFAR, DANIEL E.
 5 HUBERT, RENE S.
 6 LEONG, KAHAN
 7 RAITANO, ARTHUR B.
 8 SAFFRAN, DOUGLAS C.
 9 MITCHELL, STEPHEN CHAPPELL
 11 <120> TITLE OF INVENTION: SERPENTINE TRANSMEMBRANE ANTIGENS EXPRESSED IN HUMAN
 12 CANCERS AND USES THEREOF
 14 <130> FILE REFERENCE: 39766-0160D2
 16 <140> CURRENT APPLICATION NUMBER: US 10/750,262A
 17 <141> CURRENT FILING DATE: 2003-12-31
 19 <150> PRIOR APPLICATION NUMBER: US 10/011,095
 20 <151> PRIOR FILING DATE: 2001-12-06
 22 <150> PRIOR APPLICATION NUMBER: US 09/323,873
 23 <151> PRIOR FILING DATE: 1999-06-01
 25 <150> PRIOR APPLICATION NUMBER: US 60/087,520
 26 <151> PRIOR FILING DATE: 1998-06-01
 28 <150> PRIOR APPLICATION NUMBER: US 60/091,183
 29 <151> PRIOR FILING DATE: 1998-06-30
 31 <160> NUMBER OF SEQ ID NOS: 37
 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1195
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Homo sapiens
 40 <400> SEQUENCE: 1
 41 ccgagactca cgggtcaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60
 42 aattaatgga aagcagaaaa gacatcacaa accaagaaga actttggaaa atgaagccta 120
 43 ggagaaattht agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180
 44 aaagacctgt gcttttgcac ttgcacacaa cagcccatgc tgatgaattht gactgccctt 240
 45 cagaacttca gcacacacag gaactctttc cacagtggca cttgccaat aaaatagctg 300
 46 ctattatagc atctctgact tttctttaca ctcttctgag ggaagtaatt cacccttttag 360
 47 caacttccca tcaacaatat tttataaaaa ttccaatcct ggtcatcaac aaagtcttgc 420
 48 caatggtttc catcactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480
 49 tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540
 50 taacaagaaa gcagtttggg cttctcagtt tcttttttgc tgtactgcat gcaatttata 600
 51 gtctgtctta ccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660
 52 aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720
 53 atgtgtctct gggaattgtg ggattggcaa tactggctct gttggctgtg acatctattc 780
 54 catctgtgag tgactctttg acatggagag aatttcacta tattcagagc aagctaggaa 840
 55 ttgtttccct tctactgggc acaatacacg cattgattht tgcttggaa aagtggatag 900
 56 atataaaaaca atttgtatgg tatacacctc caacttttat gatagctgtt ttccttccaa 960
 57 ttgttgcct gatattttaa agcatactat tcttgccatg cttgaggaag aagatactga 1020

CP8-6)

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58 agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt      1080
59 tgtagaatta ctgtttacac acatttttgt tcaatattga tatattttat caccaacatt      1140
60 tcaagtttgt atttgtaaat aaaatgatta ttcaaggaaa aaaaaaaaaa aaaaa      1195
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 339
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
67 <400> SEQUENCE: 2
68 Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
69 1 5 10 15
70 Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
71 20 25 30
72 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
73 35 40 45
74 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
75 50 55 60
76 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
77 65 70 75 80
78 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
79 85 90 95
80 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
81 100 105 110
82 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
83 115 120 125
84 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
85 130 135 140
86 Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
87 145 150 155 160
88 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
89 165 170 175
90 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
91 180 185 190
92 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
93 195 200 205
94 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
95 210 215 220
96 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
97 225 230 235 240
98 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
99 245 250 255
100 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
101 260 265 270
102 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
103 275 280 285
104 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
105 290 295 300
106 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
107 305 310 315 320
108 Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys

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109          325          330          335
110 Ser Gln Leu
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 111
115 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 3
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120 attgaacatt ccagatacct atcattactc gatgctgttg ataacagcaa g.                  111
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 24
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Primer
130 <400> SEQUENCE: 4
131 actttgttga tgaccaggat tgga                                          24
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 24
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Primer
141 <400> SEQUENCE: 5
142 cagaacttca gcacacacag gaac                                          24
144 <210> SEQ ID NO: 6
145 <211> LENGTH: 3627
146 <212> TYPE: DNA
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 6
150 ggggcccgc cctctgggca gcagcggcag ccgagactca cgggtcaagct aaggcgaaga      60
151 gtgggtggct gaagccatac tattttatag aattaatgga aagcagaaaa gacatcacaa      120
152 accaagaaga actttggaaa atgaagccta ggagaaatgt agaagaagac gattatttgc      180
153 ataaggacac gggagagacc agcatgctaa aaagacctgt gcttttgcac ttgcacacaa      240
154 cagcccatgc tgatgaattt gactgccctt cagaacttca gcacacacag gaactctttc      300
155 cacagtggca cttgcccaatt aaaatagctg ctattatagc atctctgact tttctttaca      360
156 ctcttctgag ggaagtaatt cacccttag caacttcca tcaacaatat tttataaaaa      420
157 ttccaatcct ggtcatcaac aaagtcttgc caatggtttc catcactctc ttggcattgg      480
158 tttacctgcc aggtgtgata gcagcaattg tccaacttca taatggaacc aagtataaga      540
159 agtttccaca ttggttgat aagtggatgt taacaagaaa gcagtttggg cttctcagtt      600
160 tcttttttgc tgtactgcat gcaatttata gtctgtctta cccaatgagg cgatcctaca      660
161 gatacaagtt gctaaactgg gcatatcaac aggtccaaca aaataaagaa gatgcctgga      720
162 ttgagcatga tgtttggaga atggagattt atgtgtctct ggggaatttg ggattggcaa      780
163 tactggctct gttggctgtg acatctattc catctgtgag tgactctttg acatggagag      840
164 aatttcacta tattcaggta aataatatat aaaataaacc taagaggtaa atcttctttt      900
165 tgtgtttatg atatagaata tgttgacttt accccataaa aaataacaaa tgtttttcaa      960
166 cagcaaagat cttatacttg ttccaattaa taatgtgctc tcctgttgtt ttccctattg      1020
167 cttctaatta ggacaagtgt ttccatagaca taaataaaag gcattaaaat attctttgtt      1080
168 tttttttttt tgtttgtttg tttttgtttt gtttgtttgt ttttttgaga tgaagtctcg      1140

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169 ctctgttgcc catgctggag tacagtggca cgatctcggc tcaactgcaac ctgcgcctcc 1200
170 tgggttcagg cgattctctt gcctcagcct cctgagtagc tgggattaca ggcacccatc 1260
171 accatgtcca gctaattttt gtatttttag tagagacagg gttttcccat gttggccagg 1320
172 ctggtctcga tctcctgacc tcaaatgata cgcccacctc ggccctccaa agtgctggga 1380
173 tgacagttgt gagccaccac actcagcctg ctctttctaa tatttgaaac ttgttagaca 1440
174 atttgctacc catctaattg gatatttttag gaatccaata tgcattggtt attatttctt 1500
175 aaaaaaata ttcttttacc tgtcacctga atttagtaat gccttttatg ttacacaaact 1560
176 tagcactttc cagaaacaaa aactctctcc ttgaaataat agagttttta tctaccaaag 1620
177 atatgctagt gtctcatttc aaaggctgct tttccagct tacattttat atacttactc 1680
178 acttgaagtt tctaaatatt cttgtaattt taaaactatc tcagatttac tgagggttat 1740
179 cttctgggtg tagattatcc ataagaagag tgatgtgcca gaatcactct gggatccttg 1800
180 tctgacaaga ttcaaaggac taaatttaat tcagtcattga aacttgccaa ttaccgttta 1860
181 tgggttagaca tctttggaaa tttccacaag gtcagacatt cgcaactatc ccttctacat 1920
182 gtccacacgt atactccaac actttattag gcatctgatt agtttgaaa gtatgcctcc 1980
183 atctgaatta gtccagtgtg gcttagagtt ggtacaacat tctcacagaa tttcctaatt 2040
184 ttgtaggttc agcctgataa ccactggagt tctttggtcc tcattaaata gctttcttca 2100
185 cacattgctc tgcctgttac acatatgatg aacactgctt ttagacttc attaggaatt 2160
186 taggactgca tcttgacaac tgagcctatt ctactatatg tacaatacct agcccataat 2220
187 aggtatacaa tacacatttg gtaaaaactaa ttttcaacca atgacatgta tttttcaact 2280
188 agtaacctag aaatgtttca cttaaaatct gagaactggt tacactacaa gttaccttg 2340
189 agattcatat atgaaaacgc aaacttagct atttgattgt attcactggg acttaagaat 2400
190 gcgcctgaat aattgtgagt tgcatttgtt ctggcaggct aatgaccatt tccagtaaag 2460
191 tgaatagagg tcagaagtcg tataaaagag gtgtgtgcag aacaccgttg agattacata 2520
192 ggtgaacaac tatttttaag caactttatt tgtgtagtga caaagcatcc caatgcaggc 2580
193 tgaatgttt catcacatct ctggatctct ctattttgtg cagacattga aaaaattgtt 2640
194 catattattt ccatgttatc agaataattg attttttaaa aacataggcc aagttcattc 2700
195 acttcattat tcatattatc aaatcagagt gaatcacatt agtcgccttc acaactgata 2760
196 aagatcactg aagtcaaatt gatttttgct ataactctca atctacctat atttaattga 2820
197 gaatctaaaa tgtacaaatc attgtgttga ttctgcagtg atcctgctat aagtaagact 2880
198 cagtccttga ttttaggtat cctgtgaaaa gcagaattaa gacaaataca caagagacaa 2940
199 agcacaaaaa ataaatatca taaggggatg aacaaaatgg tggagaaaga gtagacaaag 3000
200 tttttgatca cctgccttca aagaaaggct gtgaattttg ttcacttaga cagcttggag 3060
201 acaagaaatt acccaaaagt aagggtgagga ggataggcaa aaagagcaga aagatgtgaa 3120
202 tggacattgt tgagaaatgt gataggaaaa caatcataga taaaggattt ccaagcaaca 3180
203 gagcatatcc agatgaggta ggatgggata aactcttatt gaaccaatct tcaccaattt 3240
204 tgtttttctt ttgcagagca agctaggaat tgtttccctt ctactgggca caatacacgc 3300
205 attgattttt gcctggaata agtggataga tataaaacaa tttgtatggt atacacctcc 3360
206 aacttttatg atagctgttt tcttccaat tgtgtcctg atatttaaaa gcatactatt 3420
207 cctgccatgc ttgaggaaga agatactgaa gattagacat ggttgggaag acgtcaccaa 3480
208 aattaacaaa actgagatat gttcccagtt gtagaattac tgtttacaca catttttgtt 3540
209 caatattgat atattttatc accaacattt caagtttgta tttgttaata aaatgattat 3600
210 tcaaggaaaa aaaaaaaaaa aaaaaaa 3627
212 <210> SEQ ID NO: 7
213 <211> LENGTH: 519
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 7
218 gacttttaca aaattcctat agagattgtg aataaaacct tacctatagt tgccattact 60
219 ttgctctccc tagtatacct cgcaggctct ctggcagctg cttatcaact ttattacggc 120

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220 accaagtata ggagatttcc accttggttg gaaacctggt tacagtgtag aaaacagctt 180
221 ggattactaa gttttttctt cgctatggtc catgttgctt acagcctctg cttaccgatg 240
222 agaagggtcag agagatatatt gtttctcaac atggcttatc agcagggttca tgcaaatatt 300
223 gaaaactctt ggaatgagga agaagtttgg agaattgaaa tgtatatctc ctttggcata 360
224 atgagccttg gcttactttc cctcctggca gtcacttcta tcccttcagt gagcaatgct 420
225 ttaaaactgga gagaattcag ttttattcag tctacacttg gatatgtcgc tctgctcata 480
226 agtactttcc atgttttaat ttatggatgg aaacgagct 519

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228 <210> SEQ ID NO: 8

229 <211> LENGTH: 173

230 <212> TYPE: PRT

231 <213> ORGANISM: Homo sapiens

233 <400> SEQUENCE: 8

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234 Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile
235 1 5 10 15
236 Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala
237 20 25 30
238 Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro
239 35 40 45
240 Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser
241 50 55 60
242 Phe Phe Phe Ala Met Val His Val Ala Tyr Ser Leu Cys Leu Pro Met
243 65 70 75 80
244 Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met Ala Tyr Gln Gln Val
245 85 90 95
246 His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu Val Trp Arg Ile
247 100 105 110
248 Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu Ser Leu
249 115 120 125
250 Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg
251 130 135 140
252 Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile
253 145 150 155 160
254 Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala
255 165 170

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257 <210> SEQ ID NO: 9

258 <211> LENGTH: 322

259 <212> TYPE: DNA

260 <213> ORGANISM: Homo sapiens

262 <400> SEQUENCE: 9

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264 cagagtgtact ttacaaaat tcctatagag attgtgaata aaaccttacc tatagttgcc 120
265 attactttgc tctccctagt ataccttgca ggtcttctgg cagctgctta tcaactttat 180
266 tacggcacca agtataggag atttccacct tgggtggaaa cctgggttaca gtgtagaaaa 240
267 cagcttggat tactaagttg tttcttcgct atgggtccatg ttgcctacag cctctgctta 300
268 ccgatgagaa gggtcagagag at 322

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270 <210> SEQ ID NO: 10

271 <211> LENGTH: 183

272 <212> TYPE: DNA

273 <213> ORGANISM: Homo sapiens

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 11,56,233,250,310,326,377,398

Seq#:34; Xaa Pos. 15,74,105,122

VERIFICATION SUMMARY

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L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

M:341 Repeated in SeqNo=12

L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0

M:341 Repeated in SeqNo=34